

# FIGURE 1

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGGCCACACCAGGACTGT  
 GTTGAAGGGTGTGTTTTTTTCTTTTAAATGTAATACCTCCTCATCTTTTCTTCTTACACAGTG  
 TCTGAGAACATTTTACATTATAGATAAGTAGTACATGGTGGATAAECTTCTACTTTTAGGAGGA  
 CTACTCTCTTCTGCAGTCTTAGACTGGTCTTCTACACTAAGACACC**ATGA**AGGAGTATGTG  
 CTCTATTATTCCTGGCTTTGTGCTCTGCCAAACCTTCTTTAGCCCTTCACACATCGCACT  
 GAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATGATG  
 ATGATGATGATGAGGACCACTCTCTTTTCCAACAAGAGAGGCCAAGAAGCCATTTTTTTCCA  
 TTTGATCTGTTTCCAATGTGTCCATTGGATGTGAGTGCTATTACGAGTTGTACATTGCTC  
 AGATTTAGGTTTGACCTCAGTCCCAACCAACATTCCATTGTGATACTCGAATGCTTGATCTTC  
 AAAACAATAAAATTAAGGAAATCAAAGAAAATGATTTAAAGGACTCCTTCACTTTATGGT  
 CTGATCTGAACAACAACAAGCTAACGAAGATTACCCAAAAGCCTTTCTAACCAAAAGAA  
 GTTGCGAAGGCTGTATCTGCCCAACAATCAACTAAGTGAATACCACTTAATCTTCCCAAT  
 CATTAGCAGAACTCAGAATTCATGAAAATAAAGTTAAGAAAATACAAAAGGACACATTCAAA  
 GGAATGAATGCTTTACACGTTTTGGAATAGAGTGCAAACCTCTTGATAATAATGGGATAGA  
 GCCAGGGGCATTTGAAGGGGTGACGGTGTTCATATCAGAATTGAGAGCAAACTGACCT  
 CAGTTCCTAAAGGCTTACCACCACTTTATTGGAGCTTCACTTAGATTATAATAAAATTTCA  
 ACAGTGGAACTTGAGGATTTTAACGATACAAAGAACTACAAAGGCTGGGCCCTAGGAAACAA  
 CAAATCAGATATCGAAAATGGGAGTCTTGCTAACATACCAGTGTGAGAGAAATACATT  
 TGGAAAACAATAAACTAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATA  
 ATCTTCCTTCACTTAATTCAATTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGCC  
 AAAGATGAAGAAATCTTTATACAGTGCAATAAGTTTATTCAACAACCCGGTGAATACTGGG  
 AAATGCAACCTGCAACATTTCTGTGTGTTTTGAGCAGAATGAGTGTTCAGCTTGGGAACCTT  
 GGAATG**TAA**AATAATTAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAATCCCTACATT  
 TGGAACTCTGAACTCTATTAATAATGGTAGTATTATATATACAAGCAAAATATCTATTCTCA  
 AGTGGTAAGTCCACTGACTTATTTTATGACAAGAAAATTTCAACGGAATTTGCCAAACTATT  
 GATACATAAGGGGTTGAGAGAAAACAAGCATCTATTGCAGTTTCTTTTTCGCTACAAATGAT  
 CTTACATAAATCTCATGCTTGACCATTCTTTCTTCAACAAAAAGTAAGATATTCTTAAAT  
 TTTAACACTTTGTTATCAAGCACATTTAAAAAAGAACTGTACTGTAAATGGAATGCTTGACT  
 TAGCAAAATTTGTGCTCTTCATTGCTGTTAGAAAAACAGAATTAAACAAAGACAGTAATGT  
 GAAGAGTGCAATACACTATTCTTATCTTTAGTAACTGGGTAGTACTGTAATTATTTTAAAT  
 CATCTTAAAGTATGATTGATATAATCTTATTGAAATTACCTTATCATGTCTTAGAGCCCGT  
 CTTTATGTTTAAAACTAATTTCTAAAAATAAGCCTTCAGTAAATGTTTATTACCAACTTGA  
 TAAATGCTACTCATAAGAGCTGGTTTGGGCTATAGCATATGCTTTTTTTTTTTTAAATATT  
 ACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTCATAAAATCTGTAACCTCGCATTTT  
 AATGATCCGCTATTATAAGCTTTTAAATAGCATGAAAATGTTAGGCTATATAACATTGCCAC  
 TTCAACTCTAAGGAATATTTTGAGATATCCCTTTGGAAGACCTTGCTTGGGAAGGCGCTGGA  
 CACTAACAAATCTACACCAATTTGCTCTTCAAATCGTATGGACTGGATAACTCTGAGAAA  
 CACATCTAGTATAACTGAATTAAGCAGAGCATCAAATTAACAGACAGAAACCGAAAGCTCTA  
 TATAAATGCTCAGAGTTCTTTATGTATTCTTATTGGCATCAACATATGTAAAAATCAGAAA  
 ACAGGGAAATTTCAATAAAATATTGGTTTGAAT

03944644.03301

## **FIGURE 2**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392

<subunit 1 of 1, 379 aa, 1 stop

<MW: 43302, pI: 7.30, NX(S/T): 1

MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFFPTREPR  
SHFFPFDLFPMPFCGQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL  
TSLYGLILNNKLTKEHPKAFLLTKKLRLYLSHNQLSEIPLNPKSLAELRIHENKVKKIQ  
KDTFKGMNALHVLEMSANPLDNNGIEPGAEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD  
YNKISTVELEDFKRYKELQRLGLGNNKITDIENGLANIPRVREIHLENNKLKKIPSGLPEL  
KYLQIIFLHSNSIARVGVDNFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV  
QLGNFGM

### **Signal sequence.**

amino acids 1-15

### **N-glycosylation site.**

amino acids 281-285

### **N-myristoylation sites.**

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

### **Leucine zipper pattern.**

amino acids 154-176



## FIGURE 4

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MPSLPAPPAPLLLLGLLLLSRPARAGAPPEPPVLPFIRSEKEPLFVRGAAGCTFGGKVYALDE  
TWHPDLGQPFVGMRCVLCACEAPQWGRRTRGPRVSCNIIKECPTPACGQPRQLPGHCCQT  
CPQERSSSERQPSGLSFEYPRDPEHRSYSDRGEPGAERARGDHTDFVALLTGPRSQAVAR  
ARVSLLRSSLRFSISYRRLDRPTRIRFSDSNGSVLFHEHPAAPTQDGLVCGVWRAVPRLSRL  
LRAEQLHVALVTLLTHPSGEVWGDLIRHRALAAETFSAILTLEGPPQQGVGGITLLTSLDTE  
SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQGQLLRELQANVSAQEPGFAEVLNLTQVQEMD  
WLVLGELQMALEWAGRPGLRISGHIAARKSCDVLQSVLCGADALI PVQTGAAGSASLTLLGN  
GSLIYQVQVVGTSSEVVAMTLETKPQRDRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAHML  
LQNELFLNVGTDKDFPDGELRGHVAALPYCGHSARHDTLPVPLAGALVLPVKSQAAGHAWLS  
LDTHCHLHYEVLLAGLGSEQGTVTALLGPPGTPGPRRLKGFYGSEAQGVVKDLEPELLR  
HLAKGMASLMITTKGSPRGELRGQVHIANQCEVGGLRLEAAGAEGVRALGAPDTASAAPVV  
PGLPALAPAKPGGPRPRDPNTCCFFEGQQRPHGARWAPNYDPLCSLCTCQRRTVICDPVVC  
PPSCPHPVQAPDQCCFVCEKQDVRLDPLGLPRSRDPGEGCYFDGDRSWRAAGTRWHFVVPFF  
GLIKCAVCTCKGGTGVEHCEKVQCPRLLACAPVVRVNPTDCKQCQCPVGSAGHPQLGDPMQADG  
PRGCRFAGQWFPESQSWHPSVPPFGEMSCITCRCGAGVPHCERDDCSLPLSCGSGKESRCCS  
RCTAHRPPETRTDPELEKEAEGS

**Signal sequence.**

amino acids 1-23

**N-glycosylation sites.**

amino acids 217-221, 351-355, 365-369, 434-438

**Tyrosine kinase phosphorylation sites.**

amino acids 145-153, 778-786

**N-myristoylation sites.**

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,  
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,  
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,  
905-911

**Amidation site.**

amino acids 87-91

**Cell attachment sequence.**

amino acids 165-168

**Leucine zipper pattern.**

amino acids 315-337

## FIGURE 5

GGCGGAGCAGCCCTAGCGCCACCGTCGCTCTCGCAGCTCTCGTCGCCACTGCCACCGCCGCCCGCTCACTGCG  
TCTGTGCTCCGGCTCCCGGCCCTCCGGCCGGGCATGCGAGCCCCGCCGCCAGCGCCCGGTGGCGAGCTGCG  
TGCCCCCGCTGGCCCTGCTGCTGCTGCTGCTCGGAGCGGGGCCCGGAGGCGAGCTTCCCTGGCCAAACCGGTGGCCCG  
CCGCGCCCTTGTGTGCGCCCGGGCCGTCGCGCCGCGCAGCCCTGCCGGAATGGGGGTGTGTGCACCTCGCCCGCTG  
AGCCGGACCCGACGACCCCGGCCCGCCCGCGGAGCCTGGGTACAGCTGACACCTGCCCCGCCGGGATCTCCGGCG  
CCAACTGCGCAGCTGTTGTGCAGATCTTGTGCGCAGCAACCTTGTCAACATGGCAACTGACGAGCAGCAGCAGCA  
GCAGCAGCGCTGGCTACCTCTGCATTTGCAATGAAGGCTATGAAGTCCCAACTGTGGAACAGGCACTTCCAGTCT  
TCCCAGCCACTGGCTGGACCGAATCCATGGCACCCCGACAGCTTCAGCCTGTTCTCTACTACTCAGGAGCCTGACA  
AAATCTCGCTCGCTCTCAGGCAACGGTGACACTGCCTACCTGGCAGCCGAAAAACAGGGCAGAAAGTTGTAGAAA  
TGAAATGGGATCAAGTGGAGGTGATCCAGATATTGCTGTGGGAATGCCAGTTCTAACAGCTCTGCGGGTGGCC  
GCCTGGTATCCTTTGAAGTGCACAGAACACCTCAGTCAAGATTCCGCAAGATGCCACTGCCTCACTGATTTTGTG  
TCTGGAAGGTACGCGCCACAGGATTCACACAGTGCTCCCTCATAGATGGACGAAGTGTGACCCCTTCAGGCTT  
CAGGGGACTGTCTCCTCGAGGAGATGCTCGCCTTGGGGAATAATCACTTTATGGTTTGTGAATGATTCTG  
TGACTAAGTCTATTGTGGCTTTGCGCTTAACCTGCTGGTGGTGAAGTTCAGCCTGTGTGCGGGGAGAGTCAAG  
CAAAATGACTTGGAGTGTTCAGGAAAGGAAAAATGACCCAGGACCGTTCAGAGGCAACTTTTCTGTACCTGTG  
AGGAGCAGTACGTGGGTACTTCTGTGAAGAATACGATGCTTGCAGAGGAAACCTTGGCAAAAACACGCGAGCT  
GTATTGTAGCAAAATGAAGCAATGGGAGCAATTTCACTGTGTTTGCCTTCTGGTTATACGTGGAGAGCTTT  
GCCAGTCCAAGATTGATTACTGCATCTAGACCCATGCAGAAATGGAGCAACATGCATTTCCAGTCTCAGTGGAT  
TCACCTGCCAGTGTCCAGAAGGATCCTCGGATCTGCTTGTGAAGAAAGGTGGACCCCTGCGCCTCGTCTCCGT  
GCCAGAACACGGCACTGCTATGTGGACGGGTACACTTTACCTGCAACTGCAGCCCGGGCTTCACAGGGCCGA  
CCTGTGCCAGCTTATTGACTTCTGTGCCCTCAGCCCCGTGTCTCATGGCAGCTGCGCGACGTTGGGCACAGCT  
ACAAATCCCTCTGTGATTCAGGATTACCATGGCCTTACTGTGAGGAGGAATATAATGAGTGCCTCTCGCTCCAT  
GCCTGAATGCAGCCACCTCGCAGGACCTCGTTAATGGCTATGAGTGTGTGCTGCCGAGAAATACAAAGGAACAC  
ACTGTGAATTGTACAAGGATCCTCGCGCTAACGTCACTGCTGTAACGAGGACCTGTGTACAGCAGCAGCGCTGA  
ATGGCAGCTGCATCTGTGCAACCCGGGTTTACAGTGAAGAGTGCAGCATTGACATAAATGAATGTGACAGTAACC  
CCTGCCACCATGGTGGGAGCTGCTGGACAGCCCAATGGTTATAACTGCCACTGCCCGCATGGTTGGTGGGAG  
CAAACTGTGAGATCCACTCCAATGGAAGTCCGGGCATATGGCGGAGAGCCTCACCAACATGCCACGGCACTCCC  
TCTACATCATCATTGGAGCCCTCTCGTGGCCCTCATCTTATGCTGATCATCTGATGCTGGGGATTGGCCGA  
TCAGCCGCAATTGAATACCAAGGTTCTCCAGGCCAGCCTATGAGGAGTTCTACAATGCCGCGAGCATGCACAGCG  
AGTTCAAGCAATGCCATTGCATCCATCCGCGATGCCAGGTTTGGAAAGAAATCCCGGCTGCAATGTATGATGTGA  
GCCCCATCGCCTATGAAGATTACAGTCTGATGACAAACCTTGGTCAACAGTATTAAACTATAAATTTTTAAGAAAAATAAAGCTTAA  
CTTTTTTGGATTATTTTTCAAAAAGATGAGATACTACACTCATTTAAATATTTTTAAGAAAAATAAAGCTTAA  
GAAATTTAAAAATGCTAGCTGCTCAAGAGTTTTCAGTAGAATATTTAAGAACTAATTTTCTGCAGCTTTTAGTTTG  
GAAAAAATATTTTAAAAACAAATTTGTGAACACTATAGACGATGTTTAAATGATGCTCTCAGCTCTCTAAACTGT  
GTGCTTCTACTAGTGTGTGCTCTTTTCACTGTAGACATATCACGAGACCCAGATTAAATTTCTGTGGTTGTTTACA  
GAATAAGTCTAATCAAGAGAGAGTTTCTGTTTTCAGCTTTGAGTGGCGGCTTTCTGAGTAGAGTTGAGAAACAC  
GTACAGTAGCATATGATGTATAATAGAGTATACCCGTTACTTAAAAAGAGTCTGAAATGTTGTTTGGTGGAAA  
AGAACTAGTTAAATTTACTATTCTTCAACCGAATGAAATTAGCCTTTGCGCTATTCTGTGCATGGGTAAAGTAC  
TTATTTCTGCAGCTTTTGTGTAACCTTGTGGAACACTTCTTCGAGTTGTTTGTGTTTCTGTAACCTTCTGTAAC  
TCGAATAGGCTCAAAAACATACGTAACGAAAAGGCTAGCGAGGCAAACTCTGATGATTGTAATCTATATTT  
TCTCTTAAAAAGTCAAGGGTTCTATATTGTGAGTAATAAATTTACATTGAGTGTGTTTGTGCTTAAGAGGTAG  
TAAATGTAAGAGAGTACTGGTTCCTCAGTAGTGAGTATTCTCATAGTCAGCCTTTATTTATCTCCAGGATGTT  
TTTGTGCGTATTTGATTGATATGTGCTTCTTCTGATTCTTGCTAATTTCAACCATATGAATAAATGTGATC  
AAGTCA

## FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQLLPALALLLLLLGAGPRGSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSR  
PEPDPQHPAPAGEPGYSCTCPAGISGANCLVADPCASNPCHHGNCSSSSSSSDGYLCICN  
EGYEGPNCEQALPSLPATGWTESMAPRQLQFPVPATQEPDKILPRSQATVTLPTWQPKTGQKV  
VEMKWDQVEVPIPIACGNASSNSSAGGRLVSFEVFPQNTSVKIRQDATASLILLWKVTATGQFQ  
QCSLIDGRSVTPLQASGGLVLLEEMLALGNNHFIGFVNDSVTKSIVALRLTLVVKVSTCVPG  
ESHANDLECSGKCKCTTKPSEATFSCTCEEQYVGTFCCEEYDACQRKPCQNNASCIDANEKQD  
GSNFTCVCLPGYTGELCQSKIDYCIIDPCRNATCISLSGFTCCQCEGYFGSACEEKVDPC  
ASSPCQNNGTCTYVDGVHFTCNCSPGFTGPTCAQLIDFCALSCAHTGTCRSVGTSYKCLCDPG  
YHGLYCEEYNECLSAFCLNAATCRDLVNGYECVCLAEYKGTCHCELYKDCPANVSCNLNGATC  
DSDGLNGTICAPGFTGEECDIDINECDSPCHGGSCLDQPNGYNCHCPHGWWGANCEIHL  
QWKSGHMAESLTNMPRHSLYIIIGALCVAFILMLIILIVGICRISRIEYQGSSRPAYEEFYNN  
CRSIDSEFSNAIASIRHARFGKSRPAMYDVSPAIYEDYSPDDKPLVTLIKTKDL

**Signal sequence.**

amino acids 1-28

**Transmembrane domain.**

amino acids 641-660

**N-glycosylation sites.**

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,  
375-379, 442-446, 549-553, 564-568

**Glycosaminoglycan attachment site.**

amino acids 320-324

**Tyrosine kinase phosphorylation sites.**

amino acids 490-498, 674-682

**N-myristoylation sites.**

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,  
373-379, 449-455, 480-486, 562-568, 565-571

**Amidation site.**

amino acids 702-706

**Aspartic acid and asparagine hydroxylation site.**

amino acids 520-532, 596-608

**EGF-like domain cysteine pattern signatures.**

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,  
491-503, 529-541, 567-579, 605-617



0946-7814

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA  
CCCCCTTTTCAGGCTTTTCAGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA  
ATCAGCTTTATTGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT  
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTT  
AGGAAAAGGAAAAATGCCACCAAGCCGTGAGAGCAACTTTTTCTGTACTCTGTGAGGAGC  
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC  
GCGAGCTGTATTGATGCAAAATGAAAAGCAAGATGGGAGCAATTTCACTGTGTTTGCCTTCC  
TGTTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT  
GAGATAGGGGAG



## FIGURE 9

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTGCCAGCCTGTAACCTGTGCCTACACCACGCCAG  
GCCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCAGAGCCCACACCATGCCGGGCACCTAC  
GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCT  
GATGCGGGACTTCCCCTCGTGGACGGCCACAACGACCTGCCCTTGGTCTTAAGGCAGTTT  
ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTTAGCTACGGCCAGACCAGCCTGGAC  
AGGCTTAGAGATGGCCTCGTGGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA  
GGACCGGGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATACGCCGATGTGTGCCT  
CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC  
TGCTCATCGGTGTAGAGGGTGGCCACTCGTGGACAATAGCCTCTCCATCTTACGTACCTT  
CTACATGCTGGGAGTGCGCTACCTGACGCTCACCCACACCTGCAACACACCTGGGCAGAGA  
GCTCCGCTAAGGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAG  
AAGGTGGTGGCAGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGC  
TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCACTCGGTGCC  
GGGTGTGTGCAACAGTGTCTCGGAATGTTCTGATGACATCCTGCAGCTTCTGAAGAAGAAC  
GGTGGCGTCTGTATGGTGTCTTTGTCCATGGGAGTAATACAGTGAACCCATCAGCCAATGT  
GTCCACTGTGGCAGATCACTTCGACCACATCAAGCTGTCTATTGGATCCAAGTTCATCGGGA  
TTGGTGGAGATTATGATGGGGCCGGCAAATTCCTCAGGGGCTGGAAGACGTGTCCACATAC  
CCGGTCTGTATAGAGAGTTGCTGAGTCTGGCTGGAGTGAAGAGCTTTCAGGGTGTCTCT  
TCGTGGAAACCTGCTGCGGGTCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGC  
AAAGCCCCCTTGGAGGACAAGTTCCTGGATGAGCAGCTGAGCAGTTCCTGCCACTCCGACCTC  
TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACCTCACTGAGATTCCCATACA  
CTGGACAGCCAAAGTTACCAGCCAAGTGGTCAGTCTCAGAGTCTCCCCCACATGGCCCCAG  
TCCTTGCAAGTTGTGGCCACCTTCCAGTCTTATTCTGTGGCTCTGATGACCCAGTTAGTCC  
TGCCAGATGTCACTGTAGCAAGCCACAGACACCCCAAAAGTTCCTGTTGTGCAGGCACA  
AATATTTCTGAAATAAATGTTTTGGACATAG

0944544-033101

## **FIGURE 10**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595

<subunit 1 of 1, 433 aa, 1 stop

<MW: 47787, pI: 6.11, NX(S/T): 5

MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG  
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALND  
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL  
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ  
LLKKNGGVVMVSLSMGVIQCNPNSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE  
DVSTYPVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS  
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLAVVATFPVLILWL

### **N-glycosylation sites.**

amino acids 58-62, 123-127, 182-186, 273-277

### **N-myristoylation sites.**

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

### **Renal dipeptidase active site.**

amino acids 134-157

## **FIGURE 11**

AAAACCTATAAAATATTCCGGATTATTCCATACCGTCCCACCATCGGGCGCGGATCCGCGGCCG  
CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA  
CCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGATGCGGGACTTCCGCTCGTGGACGGCCAC  
AACGACCTGCCCTGGTCTTAAGGCAGGTTTACCAGAAAGGGCTACAGGATGTTAACCTGCG  
CAATTTCACTACGGCCAGACAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCGCCAGT  
TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTCACCCTGGAG  
CAGATGACCTCATAAGCCGCATGTGTGCCTCCTATTCTGAGCTGGAGCTTGTGACCTCGGC  
TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGGCCACTCGC  
TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGGAGTGCCTACCTGACGCTC  
ACCCACACCTGCAACACACCCCTGGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTTCTACAA  
CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGTGGTGGCAGAAATGAACCGCCTGGGCA  
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTACAG  
GCACCTGTGATCTTCTCCCACTCGGCTGCCGGGGTGTGTGCAACAGTGCTCGGAATGTTCC  
TGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTTGTCCATGG  
GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTTCGACCACATC  
AAGGCTGTCAATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCGGCAAATT  
CCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCTGATAGAGGAGTTGCTGAGTCGTG  
GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTCGTGGAACCTGCTGCGGGTCTTCAGACAA  
GTGGAAGAGGTACAGGAAGAAAAAAATGGCAAAGCCCCCTTGAGGACAAGTTCCCGGATGA  
GCAGCTGAGCAGTTCCTGCCACTCCGACCTCTCAGCTCTGCGTCAGAGACAGAGTCTGACTT  
CAGGCCAGGAACTCACTGAGATTCCATACACTGGACAGCCAAGTTACCAGCCAAGTGGTCA  
GTCTCAGAGTCTCCCCCACCCTGACAAAACCTCACACATGCCACCCTGCCAGCACCTGA  
ACTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACAC

## **FIGURE 12**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872
><subunit 1 of 1, 446 aa, 0 stop
><NX(S/T): 5
MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQLPVI FSHSAARGVCNSARNVPPDILQ
LLKKNGGVVMVLSMGV IQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPLIEELLSRGWSEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIP IHWTAKLPKWSVSESSPHPKTHTCPPCPAPELLGGP
SVFLFPPKPKDT
```

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## FIGURE 13

CGCCAGCGACGTGCGGGCGGCTGCGCCGCGCCCTCCCGCGCCCGGCGCTGCGTCCCGCGCC  
CTGCGCCACCGCGCCGAGCCGCGAGCCCGCGCGCCCCCGGCAGCGCCGGCCCCATGCCC  
GCCGGCCCGCGGGCCCCCGCCGCCAATCCGCGCGGCGCGCCCGCGCTGTGCTGCCCCCTGCT  
GCTGTGCTCTGCGTCCCTCGGGGCGCGCGAGCCGATCAGGAGCCACACAGCTGTGATCA  
GTCCCGAGGATCCACGCTTCTCATCGGCTCCTCCTGTGCGCCACCTGCTCAGTGACCGGA  
GACCCACCAGGAGCCACCGCCGAGGGCCTCTACTGGACCCCTCAACGGGCGCGCCTGCCCCC  
TGAGCTCTCCCGTGACTCAACGCCTCCACCTTGGCTCTGCGCCTGGCCAACTCAATGGGT  
CCAGGCGCGGTGCGGGGACAACCTCGTGTGCCACGCCCGTGACGGCAGCATCCTGGCTGGC  
TCCTGCCTCTATGTTGGCCTGCCCCCAGAGAAACCCGTCAACATCAGCTGCTGGTCCAAGAA  
CATGAAGGACTTGACCTGCGCTGGACGCCAGGGGCCACCGGGGAGACCTTCTCCACACCA  
ACTACTCCCTCAAGTACAAGCTTAGGTGGTATGGCCAGGACAACACATGTGAGGAGTACCAC  
ACAGTGGGGCCCCACTCCTGCCACATCCCCAAGGACCTGGCTCTCTTTACGCCCTATGAGAT  
CTGGGTGGAGGCCACCAACCGCCTGGGCTCTGCCCGCTCCGATGTACTCACGCTGGATATCC  
TGGATGTGGTGACCACGGACCCCCCGCCGACGTGCACGTGAGCCGCGTGGGGGCGCTGGAG  
GACCAGCTGAGCGTGCCTGGGTGTCGCCACCCGCCCTCAAGGATTTCTCTTTCAAGCCAA  
ATACCAGATCCGCTACCGAGTGGAGGACAGTGTGGAAGTGAAGTGGTGGACGATGTGAGCA  
ACCAGACCTCCTGCCGCTGGCCGCCCTGAAACCCGGCACCGTGTACTTCTGTGCAAGTGCCT  
TGCAACCCCTTTGGCATCTATGGCTCCAAGAAAGCCGGGATCTGGAGTGAGTGGAGCCACCC  
CACAGCCGCTCCACTCCCGCAGTGAGCGCCCGGGCCCGGGCGCGGGGCGTGCAACCGC  
GGGGCGGAGAGCCGAGCTCGGGGCGGTGCGGCGCGAGCTCAAGCAGTTCCTGGGCTGGCTC  
AAGAAGCACGCGTACTGTCCAACTCAGCTTCCGCTCTACGACCAGTGGCGAGCCTGGAT  
GCAGAAGTCGCACAAGACCCGCAACCCAGGACGAGGGGATCCTGCCCTCGGGCAGACGGGGCA  
CGGCGAGAGGTCTGCCAGATTAAGCTGTAGGGGCTCAGGCCACCCTCCCTGCCACGTGGAGA  
CGCAGAGGCCGAACCCAACTGGGGCCACCTCTGTACCTCACTTACGGGCACCTGAGCCAC  
CCTCAGCAGGAGCTGGGGTGGCCCTGAGCTCCAACGGCCATAACAGCTCTGACTCCCAGT  
GAGGCCACCTTTGGGTGCACCCAGTGGGTGTGTGTGTGTGTGTGAGGGTGTGGTTGAGTTGC  
TAGAACCCCTGCCAGGCTGGGGGTGAGAAGGGGAGTCATTACTCCCCATTACCTAGGGCC  
CCTCCAAAAGAGTCCTTTTAAATAAATGAGCTATTTAGGTGCTGTGATTGTGAAAAA  
AAA

CGCCAGCGACGTGCGGGCGGCTGCGCCGCGCCCTCCCGCGCCCGGCGCTGCGTCCCGCGCC

## **FIGURE 14**

><ss.DNA38113

><subunit 1 of 1, 422 aa, 1 stop

><MW: 46302, pI: 9.42, NX(S/T): 6

MPAGRRGPAAQSARRPPPLLLPLLLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATCSV  
HGDPPGATAEGLYWTLNGRRLLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSIL  
AGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQDNTCEE  
YHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVS RVGG  
LEDQLSVRVVSPALKDFLFQAKYQIRYRVEDSVDWKVVDVSNQTSCLAGLKP GTVYFVQ  
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLG  
WLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGPAR

### **Signal sequence.**

amino acids 1-30

### **Transmembrane domain.**

amino acids 44-61

### **N-glycosylation sites.**

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 413-417

### **N-myristoylation sites.**

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,  
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

### **Amidation site.**

amino acids 3-7, 79-83, 411-415

### **Growth factor and cytokines receptors family signature 2.**

amino acids 325-331

# 2019年12月

[illegible]

## **FIGURE 16**

</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436

<subunit 1 of 1, 300 aa, 1 stop

<MW: 32964, pI: 9.52, NX(S/T): 1

MKFLLDIILLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQAQ

### **Signal sequence.**

amino acids 1-19

### **Transmembrane domain.**

amino acids 170-187

### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 30-34, 283-287

### **N-myristoylation sites.**

amino acids 43-49, 72-78, 122-128, 210-216



**Q&A**

GACTAGTTCCTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCCAGGACTC  
GGGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGGAGAAGCGCGGGGGCTGGAGCACCACCAA  
CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGAGCCGGGAGGGGGGACT  
GCGAGAGGACCCCGGCGTCCGGGCTCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCCTGC  
TGCTCCTGGGCTTGGCGGCCGGCTCGCCCCACTGGACGACAACAAGATCCCAGCCTCTGC  
CCGGGGCACCCCGGCCCTTCAGGCACGCGGGGCCACCATGGCAGCCAGGGCTTGGCGGGCCG  
CGATGGCCCGCAGCGCCGCGACGGCGCGCCCGGGCTCCGGGAGAGAAAGGCAGGGCGGGA  
GGCCGGGACTGCGGGGACCTCAGAGGGACCCCGGGCCGCGAGGAGAGGCCGGGACCCGCGGG  
CCCACCGGGCTGCCGGGGAGTGCTCGGTGCCCTCCGCGATCCGCCCTTCAGCGCCAAGCGCTC  
CGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCCTTGCCCTTCGACCCGCGTGCTGGTGAACG  
AGCAGGGACATTACGACGCCCTCACCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTAC  
TTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGA  
ATCCATTGCTCTTTCTTCCAGTTTTTTCGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGG  
GGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTAC  
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTTCTCCGATTCTTGGTGTACTCCGA  
CTGGCACAGCTCCCCAGTCTTTGCTTAGTGCCCACTGCAAGTGAGCTCATGCTCTCACTCC  
TAGAAGGAGGGTGTGAGGCTGACAACCAGTTCATCCAGGAGGGCTGGCCCCCTTGAATATT  
GTGAATGACTAGGAGGTGGGGTAGAGCACTCTCCGTCTGCTGCTGGCAAGGAATGGGAAC  
AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGCGAGTGGCTGGATTCTGCCCAAGACCA  
GAGGAGTGTGCTGTGCTGGCAAGTGTAAGTCCCCAGTTGCTCTGGTCCAGGAGCCACGGT  
GGGGTGCTCTCTTCTGGTCTCTGCTTCTCTGGATCTCCCCACCCCTCTGCTCTGGG  
GCCGGCCCTTTCTCAGAGATCACTCAATAAACCTAAGAACCCTCATAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAA

00914910

00914910

[illegible][illegible]

09-10-2016

09-10-2016

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09-10-2016

09-10-2016

09-10-2016

09-10-2016

## FIGURE 19

CTCTTTTGTCCACCAGCCAGCCGCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG  
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCAACAGACCCAT  
GCTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTTG  
GCACCACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC  
CTGAACAGGAAGGAGAGTTTCTTGCTCCTCTCCTTGCAACAACCGCTGCGCAGCTGGGTCCA  
GCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAG  
CCAGGGCAGCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCCGGCCTGTGGCGCACCCCTG  
CAAGTGGGCTGGAACATGCAGCTGCTGCCCGGGGCTTTGGCGTCTTTGTGTAAGTGGTCAG  
CCTATGGTTTGACAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAACGCCA  
CCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGGGGGCAC  
CTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTGCCTACTCCCCGGAGGCAA  
CTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGAAGGGTGCCTGGTGTTCGCTCTGCA  
CAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGGCTCTGTGAGGTCCCC  
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTG  
CCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGC  
ACGGCCGGTTCGGGAGGAGGAGTGTCTGTCGTCTGTGACATCGGTACGGGGAGCCACG  
TGTGCCACCAAGGTGCATTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT  
CATGGTGTCTTCAGAGGCAGACCTATTACAGAGCCAGGATGAAATGTGAGAGAAAGGCG  
GGGTGCTGGCCAGATCAAGAGCCAGAAAGTGACGACATCTCGCCTTCTATCTGGGCCGC  
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACCTCTGGATCGGGCT  
CACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTACCA  
GTTTGTGCTTTGGGCAGCCTGACAACACGGGCTGGTGTGGCTGAGTGTGCCATGGGGTTT  
GGCAACTGCGTGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAAC  
CCGAAACCGTTACATCTGCCAGTTGCCAGGAGACATCTCCCGTGGGGCCAGGGTCTT  
GAGGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGC  
CCACCTGTCTGGAACAAGGCCAGGTTAAGACCACATGCCTCATGTCCAAGAGGTCTCAGA  
CCTTGCACAATGCCAGAAGTTGGGCAGAGAGGCGAGGGAGCCAGTGAGGGCCAGGGAGTG  
AGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGA  
TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAAGGCTGCTCTCTTCCACCTGGCCAGAC  
CCTGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCACGGGGTATTAAATATGAATCAG  
CTGAAAAAAAAAAAA

## **FIGURE 20**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176

<subunit 1 of 1, 455 aa, 1 stop

<MW: 50478, pI: 8.44, NX(S/T): 2

MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWV  
QPPAADMRRLDWSLSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV  
SLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCCGRHLCAGQTAIEAFVCAYSPPG  
NWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTCH  
CHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFHTCDLRIDGDC  
FMVSSEADTYRARMKCQRKGGVLAQIKSQKVDILAFYLGRLTTNEVTDSDFETRNFWIG  
LTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFNGCVELQASAAFNWNRQCK  
TRNRYICQFAQEHISRWGPGS

### **Signal sequence.**

amino acids 1-26

### **Transmembrane domain.**

amino acids 110-124

### **N-glycosylation sites.**

amino acids 144-148, 243-247

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 45-49

### **N-myristoylation sites.**

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,  
288-294, 331-337, 398-404

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 204-215

### **EGF-like domain cysteine pattern signature.**

amino acids 249-261, 280-292

### **C-type lectin domain signature.**

amino acids 417-442

## FIGURE 21

CGGACGCGTGGGCTGGGCGCTGCAAAAGCGTGTCCC GCCGGGTCCCCGAGCGTCCCGCGCCCT  
CGCCCCCGCCATGCTCCTGCTGCTGGGGCTGTGCCTGGGGCTGTCCCTGTGTGTGGGGTCGCA  
GGAAGAGGCGCAGAGCTGGGGCCACTCTTCGGAGCAGGATGGACTCAGGGTCCCGAGGCAAG  
TCAGACTGTGTGCAGAGGCTGAAAAACCAACCTTTGATGACAGAAATTCAGTGAAGTCTACC  
ATCATTTCCTCGTTATGCTTCACTACGGTTTCTG CAGAATGCTGAACAGAGCTTCTGAAGA  
CCAGGACATTGAGTTCCAGATGCGAGATTCAGCTGCAGCTTTTCATCACCACCTTCACTATGC  
TTATTGGAGACAAGGTGTATCAGGGCGAAATTACAGAGAGAGAAAAAGAGTGGTGTATAGG  
GTAAAGAGAGAAAAGAAATAAAACACAGAAAGAAATGGAGAGAGAGGGGACTGAAATATTAG  
AGCTTCTGCAGTGATTTCCAGCAAGGACAAGGCGCCCTTTTCTCTGAGTTATGAGGAGCTTC  
TGCAGAGGCGCTTGGGCAAGTACGAGCACAGCATCAGCGTGC GGCCCCAGCAGCTGTCCGG  
AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCC  
GCTTCACAACAGCAGGCGAGAGGGGCAGTGGGCGCGGGGAAGATGATTCTGGGCCCTCCCCAT  
CTACTGTCTATTAACCAAAATGAAACATTTGCCAACATAATTTTAAACCTACTGTAGTACAA  
CAAGCCAGGATTGCCAGAATGGAATTTTGGGAGACTTTATCATTAGATATGACGTCAATAG  
AGAACAGAGCATTTGGGGACATCCAGGTTCTAAATGGCTATTTTGTGCACTACTTTGTCTCTA  
AAGACCTTCTCTCTTACCAAGAATGTGGTATTCTGTGCTTGACAGCAGTGCTTCTATGGTG  
GGAACCAAACTCCGCGAGACCAAGGATGCCCTCTTCACAATTCTCCATGACTCCGACCCCA  
GGACCGTTTTCAGTATCATTGGATTTTCCAACCGGATCAAAGTATGGAAGGACCACTTGATAT  
CAGTCACTCCAGACAGCATCAGGATGGGAAAGTGATCATTACCATATGTCAACCACTGGA  
GGCAGACATCAACGGGGCCCTGCACAGGGCCATCAGGCTCTCAACAAGTACGTGGGCCA  
CAGTGGCATTGGAGACCCGAGCGGTGCTCCTCATCGTCTTCTGACGGATGGGAAGCCACGG  
TCGGGGAGAGCGCACCTCTCAAGATCTCAACAACCCCGAGAGGCCCGCCGAGGCCAAGTC  
TGCACTCTCACCATTGGCATCGGCAACGACGTGGACTTCAGGCTGTGAGAGAACTGTCTGT  
GGAGAACTGTGGCTTCAACGGCGCGTGCACGAGGAGGAGGACGAGGCTCGCAGCTCATCG  
GGTTCTACGATGAAATCAGGACCCGCTCTCTCTGACATCCGCATCGATTATCCCCCAGC  
TCAGTGGTGCAGGCCACCAAGACCTGTTCCCCAACTACTTCAACGGCTCGGAGATCATCAT  
TGCGGGGAAGCTGTGTGGACAGGAAGCTGGATCACTGACGTGGAGGTCAACGCCAGCAACA  
GTAAGAAATTCATCATCTGAAGACAGATGTGCTGTGCGGCCCTCAGAAGGCGAGGAAAGAT  
GTCACAGGAAGCCCCAGGCTTGGAGGCGATGGAGAGGGGACACCAACCCATCGAGCGTCT  
CTGGAGTACCTCACCACAAGGAGCTGCTGAGCTCCTGGCTGCAAAGTGACGATGAACCGG  
AGAAGAGGCGGCTGCGGAGCGGGCCAGGCCCTGGCTGTGAGCTACCGCTTCCTCACTCCC  
TTCACCTCCATGAAGCTGAGGGGGCCGCTCCACGCATGGATGGCCTGGAGGAGGCCACGG  
CATGTGCGCTGCCATGGGACCCGAACCGGTGGTGCAGAGCGTGCAGGAGGCTGGCACGCGAC  
CAGGACCTTTGCTCAAGAAGCCAAACTCCGTCAAAAAAAACAAAAACAAAAACAAAAAGCA  
CATGGAGAGATGGTGTTTTCTCTCCACCACTGGGGATACGATGAAGAAGATGGCCACCT  
GCAAGCCAGGAAGACGGCCCTCACCAGACACCATGTCTGTGACCTTGATCTTGGACCTC  
CGAGCTTCAGAACTGTGAGAAATAAATGTGTTTGAAGCTAAAAAAGAAAAAAGAAAAA  
AAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

## **FIGURE 22**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192

<subunit 1 of 1, 694 aa, 1 stop

<MW: 77400, pI: 9.54, NX(S/T): 6

MLLLGLCLGLSLCVGSQEAAQSWGHSSEQDGLRVPRQVRLLRKTKPLMTEFSVKSTIIIS  
RYAFTTVSCRMLNRASEDQDIEFQMQUIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKE  
KRNKTTEENGEKGTEIFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLS  
VDVNILESAGIASLEVLP LHN SRQSGRGEDDSGPPPSTVINQNETFANIIFKPTVVQQAR  
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFLDSSASVMGTK  
LRQTKDALFTILHDLRPQDRFSIIIGFSNRKIVWKDHLISVTPDSIRDGKVYIHHMSPTGGTD  
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNTREAARGQVCIF  
TIGIGNDVDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV  
QATKTLFPNYPNGSEII IAGKLVDRLDHLHVEVTASNSKKFIILKTDVPVRPQKAGKDV TG  
SPRPGDGEGDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS  
MKLRGPVPRMDGLEAHGMSAAMGPEPVVQSVRGAGTQPGFLLKKPNSVKKKQNKTKKRHRG  
DGVFPLHHLGIR

### **Signal sequence.**

amino acids 1-14

### **N-glycosylation sites.**

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

### **Glycosaminoglycan attachment sites.**

amino acids 213-217, 391-395

### **N-myristoylation sites.**

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

## **FIGURE 23**

CGGACGCGTGGGGTGCCCGACATGGCGAGTGTAGTGTCTGCCGAGCGGATCCAGTGTGCGGC  
GGCAGCGGCGGCGGCGGCCCTCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCCGCGG  
CACTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGA  
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTACAGTACTGAA  
TCCCAACAGGCAGACCATTATTTCAGGGACTTCAGGCCCTTTGAAGGACAGCAGGTTTCAGT  
TGCTGAATTTTCTAGCAGTGAACCTCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAA  
GGAAGATACTTTTGCCAGCTCTATACCGATCCCCACAGGAAAGTTACACCACCATCACAGT  
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG  
AGATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAA  
GGGAACACAGAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACTGTGAC  
CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGG  
AGCACCTGCGGTCACCTGGAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT  
CAAGTGACATTCAGATGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGA  
GTTAACATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGGTAACTTGGGTGAGAGTCGATG  
ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCCAACCTGTTTCATCAATAACCTAAACAAA  
ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGGAAGCTCACTCGGATTA  
TATGCTGTATGTATACGATCCCCCACAACCTATCCCTCCTCCACAACAACCACCACCACCA  
CCACCACCACCACCACCATCCTTACCATCATCACAGATTCCCGAGCAGGTGAAGAAGGC  
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTCTGTGGCGGTGGTGGTTCGCCAT  
GCTGTGCTTGCTCATATTCTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTC  
ATGAAGCCAAAGGAGCCGATGACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGA  
GGACAGAACAACCTCCGAAGAAAAGAAAGAGTACTTCATCTAGATCAGCCCTTTTGTGTTCAAT  
GAGGTGTCCAACCTGGCCCTATTTTAGATGATAAAGAGACAGTGATATTGG

## **FIGURE 24**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518  
<subunit 1 of 1, 440 aa, 1 stop  
<MW: 48240, pI: 4.93, NX(S/T): 7  
MASVVLPSGSQCAAAAAAAPPGLRLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISC  
QVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSELKVSILNVSISDEGRYFCQL  
YTDPPQESYTTITVLVPPRNLMDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKG  
KSEVEEWSDMYTTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPVVHIQMT  
YPLQGLTREGDALELTCEAIGKPQPMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYR  
CEASNIVGKAHSDYMLYVYDPPTTIPPTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDH  
AVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEE  
KKEYFI

### **Signal sequence.**

amino acids 1-36

### **Transmembrane domain.**

amino acids 372-393

### **N-glycosylation sites.**

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,  
430-434

### **Tyrosine kinase phosphorylation sites.**

amino acids 233-240, 319-328

### **N-myristoylation sites.**

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,  
411-417, 427-433, 428-432



## FIGURE 25

GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCCGA  
CCCGCCAGGAAAGACTGAGGCGCGCGCCTGCCCGCCCGGCTCCCTGCGCCGCGCGCGCCTC  
CCGGGACAGAAGATGCTGCTCAGGGTCCCTCTGCTGCTGCGGTGCTCCTGCTACTGGCCCT  
GGGGCTTGGGTGACAGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCT  
GCACTGCCCGCCAGGGGACCAACGGTGCCCGGAGACGTGCCACCCGACACGGTGGGGCTGTAC  
GTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCGGGCTGCCGGGCTGCA  
GCTCTGGACCTGTACAGAAACAGATCGCCAGCCTGCGCTGCCCGCCTGCTGCTGCTGG  
ACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCGGCATCCTGGACACTGCCAACGTGGAG  
GCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGG  
CAACCTCCACGACCTGGATGTGTCCGACAACCAAGCTGGAGCGAGTGCACCTGTGATCCGAG  
GCCTCCGGGGCTGACGCGCTGCGGCTGGCCGGCAACACCCGATTGCCAGCTGCGGCC  
GAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGC  
CCTGCTTGGCGACCTCTCGGGCTCTTCCCGCCTGCGGCTGCGGAGCTGCCCGCAAC  
CCTTCAACTGCGTGTGCCCTTGAGCTGGTTTGGCCCTGGGTGCGCGAGAGCCACGTCA  
CTGGCCAGCCTGAGGAGACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCT  
GGAGCTTGACTACGCCGACTTTGGCTGCCCGAGCCACCACCACAGCCACAGTGCACCA  
CGAGGCCCGTGGTGGCGGAGCCACAGCCTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGC  
CCACAGCGCCGGCCACTGAGGCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGC  
TGTCGCCAGCCCGAGGATGCCACCGTCCACCTGCTCAATGGGGGCACATGCCACCTGG  
GACACCGCCACCACTGGCGTGTGTGTGCCCGAAGGCTTCAAGGCTGTACTGTGAGAG  
CAGATGGGGCAGGGGACAGGCCAGCCCTACACAGTCAAGCCGAGGCCACCACGGTCCCT  
GACCTGGGCATCGAGCCGGTGCAGCCCCACCTCCTGCGCGTGGGGCTGCAGCGCTACCTC  
AGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT  
AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACAGGTCACCCAGTGGC  
GCCAACGCCACTTACTCCGTCTGTGTATGCTTTGGGGCCCGGGCGGGTCCCGAGGGCG  
AGGAGGCTGCGGGGAGGCCATACACCCAGCCGTCCACTCAACACCGCCAGTCAAC  
CAGGCCCGGAGGGCAACCTGCCGCTCCTCATTTGCCCGCCCTGCGCGGCTGCTCCTGGC  
CGCGCTGGCTGCGGTGGGGGAGCCTACTGTGTGCGGCGGGGGCGGGCCATGGCAGCAGCG  
CTCAGGACAAAGGGCAGGTGGGGCCAGGGCTGGGCCCTTGGAACTGGAGGGAGTGAAGGTC  
CCCTTGAGGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCTGCTCCAGCGGGCTTGA  
GTGTGAGGTGCCACTCATGGGCTTCCAGGGCCTGGCCTCAGTCAACCCCTCCACGCAAGC  
CCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGC  
CAGCCCCCTCCTGTGCCACACCACTTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGA  
CAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAG  
ATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCGCAACCGAGTGCCATATGAGGACAGTGT  
CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGCGCTGCCATGTGCTGGTAAC  
GCATGCTGGGCCCTGCTGGGCTCTCCACTCCAGCGGACCTTGGGGCGCAGTGAAGGAAG  
CTCCCGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTCTAGTCTTTGGCCCCAGG  
AAGCGAAGGAACAAAGAAACTGGAAAGGAAGATGCTTTAGGAACATGTTTTGCTTTTTTAA  
AATATATATATATTTATAAGAGATCCTTTCCCATTTATTCTGGGAAGATGTTTTTCAAACCT  
AGAGACAAGGACTTTGGTTTTTGTAAAGACAACGATGATATGAAGGCCCTTTTGTAAAGAAAA  
ATAAAAAAAAAA

## FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVPLLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTPVRDVPDPDVGGLYVFEN  
GITMLDASSFAGLPGLQLLDLSQNIASLRIPRLLLLLDLSHNSLLALEPGILDANVEALRL  
AGLGLQQLDEGLFSLRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDLA  
GLAALQELDVSNLSLQALPGDLGSLFPRLRLAAARNPFNCVCLSWFGPWVRESHVTLASP  
EETRCHFPKPNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAP  
ATEAPSPSTAPPTVGPVPQPDCCPPSTCLNGGTCHLGRHHLACLCEGFTGLYCESQMGQ  
GTRPSPTPVTPRPPRSRLTGLIEFVSPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSPGDKRLV  
TLRLPASLAETVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQARE  
GNLPLLIAPALAAVLLAALAAVGAAYCVRRRGRAMAAAAQDKGVGPGAGPLELEGVKVPLEP  
GPKATEGGGEALPSGSECEVPLMGFFGPGGLQSPHAKPYI

### Signal sequence.

amino acids 1-23

### Transmembrane domain.

amino acids 501-522

### N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

### Tyrosine kinase phosphorylation site.

amino acids 262-270

### N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

### Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

### EGF-like domain cysteine pattern signature.

amino acids 355-367

### Leucine zipper pattern.

amino acids 122-144, 194-216

## FIGURE 27

GGCACTAGGACAACCTTCTTCCCTTCTGCACCACTGCCCGTACCCCTTACCCGCCCGCCACC  
TCCTTGCTACCCCACTCTTGAAACCAAGCTGTTGGCAGGGTCCCCAGCTCATGCCAGCCTC  
ATCTCCTTTCTTGCTAGCCCCAAAGGGCCTCCAGGCAACATGGGGGGCCAGTCAGAGAGC  
CGGCACTCTCAGTTGCCCTCTGGTTGAGTTGGGGGGCAGCTCTGGGGGCCGTGGCTTGCGCC  
ATGGCTCTGCTGACCAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA  
GGGGACAGGAGGCCCTCCAGAATGGGGAAGGGTATCCCTGGCAGAGTCTCCCGAGCAGA  
GTTCCGATGCCCTGGAAGCCTGGGAGAATGGGGAGAGATCCCGAAAAGGAGAGCAGTGCTC  
ACCAAAAAACAGAAGAAGCAGCACTCTGTCTGCACCTGGTTCCTTAACGCCACCTCCAA  
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGGCGTGGGAGAGGCCATAC  
AGGCCCAAGGATATGGTGTCGAATCCAGGATGCTGGAGTTTATCTGCTGTATAGCCAGGTC  
CTGTTTCAAGACGTGACTTTCACCATGGGTGAGGTGGTGTCTCGAGAAGGCCAAGGAAGGCA  
GGGAGACTCTATTCGATGTATAAGAAGTATGCCCTCCACCCGACCGGGCTACAACAGCT  
GCTATAGCGCAGGTGTCTTCCATTACACCAAGGGGATATTCTGAGTGTATAATTCCCCGG  
GCAAGGGCGAACTTAACCTCTCTCCACATGGAACCTTCCTGGGGTTGTGAAACTGTGATT  
GTGTTATAAAAAGTGGCTCCAGCTTGAAGACCAGGGTGGGTACATACTGGAGACAGCCAA  
GAGCTGAGTATATAAAGGAGAGGGAATGTGCAGGAACAGAGGCATCTTCCTGGGTTTGGCTC  
CCCGTTCCTCACTTTTCCCTTTTCATTCCCAACCCCTAGACTTTGATTTTACGGATATCTTG  
CTTCTGTCCCCATGGAGCTCCG

## **FIGURE 28**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27433, pI: 9.85, NX(S/T): 2

MPASSPFLAPKGPPGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTELQSLRREV  
SRLQGTGGPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRVLTQKQKKQHSVLHLVPIN  
ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREG  
QGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARA KLNLSPHGTF LGFVKL

### **Signal sequence.**

amino acids 1-40

### **N-glycosylation site.**

amino acids 124-128

### **Tyrosine kinase phosphorylation site.**

amino acids 156-164

### **N-myristoylation site.**

amino acids 36-42, 40-46, 179-185, 242-248

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 34-45

# FIGURE 29

CACTTTCTCCCTCTCTTCTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGAC  
 CTCGGAGACCGCGCCGGGAGACGGAGGTGCTGTGGGTGGGGGGACCTGTGGCTGCTCGTA  
 CCGCCCCCACCCTCTCTTCTGCACTGCCGTCTCCGGAAGACCTTTCCCTCGCTCTGTT  
 TCCCTTACCGAGTCTGTGCATCGCCCCGACCTGGCCGGGAGGAGGCTTGGCCGGCGGGAGA  
 TGCTCTAGGGGCGGCGCGGAGGAGCGGCCGGCGGGACGGAGGGCCCGGCAGGAAGATGGGC  
 TCCCGTGACAGGGACTCTTGTCTGGCGTACTGCGCTGCTCTTGGCTTTGCCTCTGGCCTGGT  
 ACTCGAGGCTGTGCCCATGTCCAGGGGGAACAGCAGGAGGAGGGGACTGAGGAGCTGC  
 CGTCGCCCTCCGGACCATGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCAGTCTAG  
 GACCAGGGGCTCCCTGCTTCCCGGTGCTTGGCTGCTGTGACCCCGGTACCTCCATGTACCC  
 GCGACCGCCGTGCCCCAGATCAACATCACATATCTTGAAGGGGAGAAGGGTGACCCGGAG  
 ATCGAGGCTTCCAAGGGAAATATGGCAAAACAGGCTCAGCAGGGGCCAGGGGCCACACTGGA  
 CCAAAGGGCAGAAGGGCTCCATGGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC  
 CTTTTCGGTGGGCCGGAAGAAGCCCATGCACAGCAACCACTACTACGAGCGGTGATCTTCG  
 ACACGGAGTTTCGTAACCTCTACGACCACTTCAACATGTTACCCGGCAAGTTCTACTGCTAC  
 GTGCCGGCCTCTACTTCTTACGCCCTCAACGTGCACACTTGAACAGAAAGGAGACCTACCT  
 GCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTCGCGCAGGTGGGGCAGCCGACGCA  
 TCATGCAAGGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACAGGTTGTGGGTACGCCCTC  
 TACAAGGGCGAACGTGAGAACGCCATCTTTCAGCGAGGAGCTGGACACCTACATCACCTTCAG  
 TGGCTACCTGGTCAAGCAGGCCACCGAGCCCTAGCTGGCCGCCACCTCTTTCTCTCGCC  
 ACCTTCCACCCCTGCGCTGTGCTGACCCCAACCGCTCTTCCCGGATCCCTGGACTCGGACTC  
 CCTGGCTTTGGCATTCAGTGAGACGCCCTGCACACAGAAAGCCAAAGCGATCGGTGCTCC  
 CAGATCCCGAGCCTCTGGAGAGAGCTGACGGCAGATGAAATACCAAGGGCGGGGCACCCGC  
 GAGAACCCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCTCAAGTGACCCCGCAGCGG  
 GATCGCGGCTGGCGGCAGGGCGTCCAGGGTGCGGCACCGCGCTCCAGTCCCTTGGAAATA  
 ATTAGGCAAAATCTAAAGGTCTCAAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGG  
 TTGTTATTTTGTCTTTCAGCCAGCCTGTGGCTCCCAAGAGAGAGCCCTTTTCAGTTGAG  
 ACTCTGTCTAAGAGAATCCAAAGTTAAAGCTCTGGGGTCAGGGGAGGGGCCGGGGCAGG  
 AAACCTACCTCTGGCTTAATTCTTTTAAAGCCAGTAGGAACCTTCTTGAGGGATAGGTGGACC  
 CTGACATCCCTGTGCCCTTGGCCCAAGGGCTCTGCTGGTCTTCTGAGTCACAGCTGCGAGGT  
 GATGGGGCTGGGGCCCCAGGCGTCAGCCTCCAGAGGGACAGCTGAGCCCCCTGGCTTGGC  
 CTAGGTTTGGTAGAAGCAGCCGAAGGGCTCTGACAGTGGCCAGGGACCCCTGGGTCCCCCA  
 GGCTTGACATGTTTTCTATGAGGGGAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC  
 ATCCCTGTGCCACCCAGAGCCCTGGGGGTGGTCTCCATGCTCTGCCACTGGCATCGGCT  
 TTTCTGTGCCCTCCACACAATCAGCCCCAGAAGGCCCGGGGCTTGGCTTCTGTTTTTT  
 TATAAAACACCTCAAGCAGCACTGCAGTCTCCATCTCCTCGTGGGCTAAGCATCACCGCTT  
 CCACGTGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCATGCCCT  
 CACGAGCCTCTGACCACTAGCTGAGAGGGGCTTTTCTAGGCTCAGAGCAGGGGAGAG  
 CTGGAAGGGGCTAGAAAGCTCCCGCTTGTCTGTTTCTCAGGCTCCTGTGAGCCTCAGTCCGT  
 AGACCAAGCTCAAGAGGAAGTACAGTCCCAATCACCCGTGTGAGGATTCACCTCTCAGGAGC  
 TGGGTGCGAGGAGGCAATAGCCCTGTGGCAATTGACAGGACAGCTGGAGCAGGGTGTGC  
 GTGTCTCCACGGTGTCTCTGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCCC  
 ATAGCCCTCTCCACCTCACCCCATGTTGATGCCAGGGTCACTCTGTGATCCCGCTGGGGC  
 CCCAAACCCCGCTGCTCTCTCTTCCCTTCCCCCATCCCCACCTGGTTTGTACTAATCTCTGC  
 TTCCCTCTCTGGGCTGGCTGCGGGATCTGGGGTCCCTAAGTCCCTCTCTTTAAAGAACTT  
 CTGGGGGTGAGACTCTGAAGCCGAGTGTCTGTGGGCGTGCCCGGAAGCAGAGCGCCACACTC  
 GCTGCTTAAAGCTCCCCAGCTCTTTCAGAAAAACATTAAGCTCAGAAATTGTGTTTTCAA

## **FIGURE 30**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234

><subunit 1 of 1, 281 aa, 1 stop

><MW: 31743, pI: 6.83, NX(S/T): 1

MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRP  
SQDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH  
TGPKGQKGSMSGAPGERCKSHYAAFVSVGRKKPMHSNHYYQTVI FDTFVNLYDHFNMFTGKFY  
CYVPGLYPFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV  
RLYKGERENAIFSEELDTYITFSGYLVKHATEP

### **Signal sequence.**

amino acids 1-25

### **N-glycosylation site.**

amino acids 93-97

### **N-myristoylation sites.**

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

### **Amidation site.**

amino acids 150-154

### **Cell attachment sequence.**

amino acids 104-107

# FIGURE 31

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGCGGATTGCGCGGTCTTCCGCGCG  
GCGCGACAGAGCTGTCTCGCACTTGGATGGCAGCAGGGGGCGCCGGGGTCTCTCGACGCCA  
GAGAGAAATCTCATCTCTGTGCGACCTTCTTAAAGCAAACCTAAGACCAAGAGGGAGGATTAT  
CCTTGACCTTTGAAGACCAAACTAAACTGAAATTTAAATAGTTCTTCCGGGGGAGAAGGGAG  
CTTGACTTACACTTTGGTAATAATTGCTTCTCGACACTAAGGCTGTCTGCTAGTCAGAATT  
GCCTCAAAAGAGTCTAGAAGATGTTGTCAATTGACATCCAGTCATCTCTTTAAGGAATC  
AGAGCAATGAGCCGATATATCTTCAACTCAAGAAGCTGCATTAAATCTTGCTGTTCAAC  
AAAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA  
GACAACCCAACTGCTACCTATTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACAGCA  
AAAGGACTTATGAGTTACAGGATAATTACAGATTTCCATCTTTGACCAGAAATTTGCCAAG  
CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAATTTTCAAGCAGTCACTCCCC  
TAGCCCATCATCACAGATTATTCAAAGCCCAACCGATATCTCATGGAGAGACACTTTCT  
CAGAAGTTTGATCTCTCAGATCACCTGGAGAAACTATTAAAGTGGATGAAGCAAGTGCCCA  
GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTACAAATTTTCTCTGATCAAGAAA  
TAGCTCATCTGCTGCTGAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA  
CATACCACCTCGGCTACTCCAAGGCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC  
TTCTGGGACTTCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAAACCACTGTCACTTCTC  
AGCCTCCACGACCTCTATTTCTACAGTTTTTACACGGGCTGCGGTACACTCCAAGCAATG  
GCTACAAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCGAGCTTAGA  
AACCATACCGTTTACAGAAATCTCCAACCTTAACCTTGAACACAGGGAATGTGTATAACCTA  
CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCGGGAAGGT  
AGGGAGGCCAGTCCAGGCAGTTCTCCAGGGCAGTGTTCCAGAAAAATCAGTACGGCCTTCC  
ATTTGAAAAATGGCTTCTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTGTTGATAGGCC  
TCGTCCTCCTGGGTAGAAATCCTTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT  
TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT  
TAGTAACCCAGAGCCCAATGCAATGAGTTTCTGCTGACTTGTAGTCTTAGCAGGAGGTTG  
TATTTTGAAGACAGGAAAAATGCCCTTCTGCTTTCTTTTTTTTTTTTGGAGACAGAGTCTT  
GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC  
CTGGGTTCAAGCGATTCTCTGCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA  
CCACACTCGGGTGATTTTGTATTTTGTAGTAGAGACGGGGTTCCACATTTGGTCAGGCTG  
GTCTCAAACCTCTGACCTAGTGATCCACCTCTCGGCTCCCAAAGTGCTGGGATTACAGG  
CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTTGGTTTTGAGAAGGAATGAAGTG  
GGAACCAAAATTAGGTAATTTTGGGTAATCTGTCTTAAATATTAGCTAAAAACAAGCTCT  
ATGTAAGTAATAAGATAAATTGCCATATAAAATTTCAAATTCACATGGCTTTTATGCAAA  
GAAACAGTTTAGGACATCTAGGTTCCAATTCAATTCATTTCTGGTTCAGATAAAATCAAC  
TGTTTATATCAATTTCTAATGGATTGCTTTTCTTTTATATGGATTCTTTAAACTTATT  
CCAGATGTAGTTCTTCCAATTAATATTGAATAAATCTTTGTTACTCAA

## **FIGURE 32**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410  
><subunit 1 of 1, 431 aa, 1 stop  
><MW: 46810, pI: 6.45, NX(S/T): 6  
MFFGEGSLTYTLVIIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED  
CINSCCSTKNISGDKACNLMI FDRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP  
SLTRNLPSQELPQEDSL LHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF  
KMDEASQQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL  
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP  
TDSKGSLETIPFTEISNLTNLNGVNYNPTALSMNSVESSTMNK TASWEGREASPGSSSQGSV  
PENQYGLPF EKWLLIGSLLFGVFLVIGLVLLGRILSES LRKRYSRLDYLINGIYVDI

### **Signal sequence.**

amino acids 1-25

### **Transmembrane domain.**

amino acids 384-405

### **N-glycosylation sites.**

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 415-419

### **Tyrosine kinase phosphorylation site.**

amino acids 50-57

### **N-myristoylation sites.**

amino acids 4-10, 48-54, 315-321



## FIGURE 33

GC GGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCTGTGGTCTTC  
GCCTCCTTGTGTGCCTGGTATTTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT  
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCTCAAAGCTCCAGTCC  
CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA  
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG  
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAAC TGGA  
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCATAACTCTGGACCGATGACAAAG  
TTTATTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC  
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA  
TGAAATTCAGGTCTAGCTGGGTATTTATTCGAGCAAAAGGCTTGGAACCTCCCTCCGAAATTC  
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAAACAACAGATATTCTGGCTGGCCTGCAGA  
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTGACACTGCAGGGTCTTGAGTAAAT  
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTCTAAATCCAACA  
GCCCATATTTGATGAGTATTTTGGGTTTGTGTAAACCAATGAACATTTGCTAGTTGTATCA  
AATCTTGGTACGCAGTATTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA  
AACTAAATGAATGGAAATTCCTAAAAA

0904151515 0904151515

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777
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><subunit 1 of 1, 235 aa, 1 stop

><MW: 25982, pI: 9.09, NX(S/T): 2

MRPLAGGLKVVFVVASLCAWSYGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK  
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT  
RCFDMYEGDNSGPMTKFIQSAAPKSLFMVITYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS  
SWVFIAAKGLELPSEIQOREKINHSDAKNNRYSGWPAEIQIEGCIPIKERS

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125